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1: AAA44992. envelope polyprot...[gi:328423]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAA44992 854 aa linear VRL 02-AUG-1993
DEFINITION envelope polyprotein.
ACCESSION AAA44992
VERSION AAA44992.1 GI:328423
DBSOURCE locus HIVNL43 accession M19921.1
KEYWORDS
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
Viruses; Retroviridae; Lentivirus; Primate lentivirus group.
REFERENCE 1 (residues 1 to 854)
AUTHORS Adachi,A., Gendelman,H.E., Koenig,S., Folks,T., Willey,R., Rabson,A. and Martin,M.A.
TITLE Production of acquired immunodeficiency syndrome-associated retrovirus in human and nonhuman cells transfected with an infectious molecular clone
JOURNAL J. Virol. 59 (2), 284-291 (1986)
MEDLINE 86281827
PUBMED 3016298
REFERENCE 2 (residues 1 to 854)
AUTHORS Buckler,C.E., Buckler-White,A.J., Willey,R.L. and McCoy,J.
JOURNAL Unpublished (1988)
REFERENCE 3 (sites)
AUTHORS Dai,L.C., West,K., Littaua,R., Takahashi,K. and Ennis,F.A.
TITLE Mutation of human immunodeficiency virus type 1 at amino acid 585 on gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T lymphocytes
JOURNAL J. Virol. 66 (5), 3151-3154 (1992)
MEDLINE 92219406
PUBMED 1373204
COMMENT [3] sites; revisions of [3].
Clean copy of sequence [3] kindly provided by Chuck Buckler, NIAID, Bethesda, MD, 24-JUN-1988. The construction of pNL4-3 has been described in [1]. pNL4-3 is a recombinant (infectious) proviral clone that contains DNA from HIV isolates NY5 (5' half) and BRU (3' half). The site of recombination is the EcoRI site at positions 5743-5748.
The length and sequence of the vpr coding region corresponds to that of the BRU, SC, SF2, MAL and ELI isolates. The vpr coding region of these isolates is about 18 amino acid residues longer than the vpr coding region of the IIIb isolates. In HIVNL43, this shift is due to a single base deletion (with respect to the IIIb's) at position 5770. The sequence at this position is 'atttc' in HIVNL43 and 'attttc' in HIVXB2.
The original BRU clone, sequenced by Wain-Hobson, et al. (Cell 40, 9-17 (1985)), and the BRU portion of the pNL4-3 recombinant clone are different clones from the same BRU isolate.
Two of the revisions reported in the FEATURES produced changes in amino acid sequences. The revision at position 2421 changes one amino acid residue from 'R' to 'G' in the pol coding region. The revision at positions 8995-9000 changes three amino acid residues from 'AHT' to 'VTP' in the nef coding region.

Method: conceptual translation.

FEATURES Location/Qualifiers

source 1..854

/organism="Human immunodeficiency virus 1"

/db_xref="taxon:11676"

Protein 1..854

/name="envelope polyprotein"

CDS 1..854

/coded_by="M19921.1:6221..8785"

ORIGIN

1 mrvkekyqhl wrwgwkwtgm llgilmicsa tekllwvtvyy gvpvwkeatt tlfcasdaka
61 ydtevhnvwa thacvptdpn pgevvlnvt enfnmwkndm veqmhediis lwdqslkpcv
121 kltplcvslk ctdlkndtnt nsssgrmime kgeikncsfn istsirdkvq keyaffykld
181 ivpidntsyr liscntsvit qacpkvsfep ipihycapag failkcnnak fngtgpcnvv
241 stvqcthgir pvvstqlnn gslaeedvvi rsanftdnak tiivqlntsv einctrpnnn
301 trksiriqrg pgafavtigk ignmrqahcn israkwnatl kqiasklreq fgnnktiifk
361 qssggdpeiv thsfncggef fycnstqlfn stwfnstwst egsnnategsd titlpcrikq
421 finmwqevgk amyappisqq ircssnitgk lltrdggnnn ngseifrpqg gdmrdrnwrs
481 lykykvvkic plgvaptkak rrrvvqrekra vgigalflgf lgaagstmgc tsmtltvqar
541 qllsdivqqq nnllraieaq qhllqltvwg ikqlgarila verylkdqql lgiwgcsqkl
601 icttavpwna swsnksleqi wnnmrtwmewd reinnytsli hslieesqnq qekneqelle
661 ldkwaslwnw fnitnwlwyi klfimivgg vglrivfafv sivnrvrqgy splsfqthlp
721 iprgpdprpeg ieeeggerdr drsirlvngs laliwddlr lclfshyhrllr dilllivtriv
781 ellgrrgwea lkywwnllqy wsqelknsav nllnataiaav aegtdrviev lqaayrairh
841 iprrirqgle rill

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1: AAB59751. envelope polyprot...[gi:326424]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAB59751 861 aa linear VRL 02-AUG-1993
DEFINITION envelope polyprotein.
ACCESSION AAB59751
VERSION AAB59751.1 GI:326424
DBSOURCE locus HIVBRUCG accession [K02013.1](#)
KEYWORDS
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
Viruses; Retroviridae; Lentivirus; Primate lentivirus group.
REFERENCE 1 (residues 1 to 861)
AUTHORS Wain-Hobson,S., Sonigo,P., Danos,O., Cole,S. and Alizon,M.
TITLE Nucleotide sequence of the AIDS virus, LAV
JOURNAL Cell 40 (1), 9-17 (1985)
MEDLINE 85099333
PUBMED 2981635
COMMENT [(in) Weiss,R., Teich,N., Varmus,H. and Coffin,J. (Eds.);RNA Tumor Viruses, Molecu] review.
[3] revision of [1].
The original LAV, sometimes called LAV-1 to distinguish it from HIV2 (LAV-2), is now referred to as HIV-1bru. An infectious clone of this virus has been constructed by Keith Peden, Molecular Biology and Genetics, Johns Hopkins University School of Medicine, Baltimore, MD 21205 (301) 955-3652. HIVNL43 is also an infectious clone having for its 3' half a clone of the BRU isolate. Acquired immune deficiency syndrome (AIDS) is caused by a retrovirus known by several different names, probably representing two separate strains: human T-cell lymphotropic virus-III (HTLV-III) and lymphadenopathy-associated virus (LAV) are thought to be one strain, and AIDS-associated retrovirus type 2 (ARV-2) the other. All three viruses, whose sequences do not differ by more than about 6%, are believed to belong to the retroviral subfamily Lentiviridae, or 'slow' viruses.
For the details of the annotation and for other pertinent references, see the HIV reference entry.
Method: conceptual translation.
FEATURES Location/Qualifiers
source 1..861 /organism="Human immunodeficiency virus 1"
/db_xref="taxon:11676"
Protein 1..861 /name="envelope polyprotein"
CDS 1..861 /coded_by="K02013.1:5803..8388"
ORIGIN

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1 mrvkekyqhl wrwgwkwtgm llgilmicsa tekliwvtvyy gvpvwkeatt tlfcasdaka
61 ydtevhnvwa thacvptdpn pqevvlvnvt enfnmwkndm veqmhedis lwdqslkpcv
121 kltpcvslk ctdlgnatnt nssntnsssg emmmekgeik ncsfnistsi rgkvqkeyaf
181 fykldiipid ndttsytlts cntsvitqac pkvsfepipi hycapagfai lkcnktfng
241 tgpctnvstv qcthgirpvv stqlllngsl aeeeenvirsa nftdnaktii vqlnqsvein
301 ctrpnnntrk siriqrgpgr afvtigkign mrqahcnisr akwnatlkqi asklreqfgn
361 nktiifkqss ggdpeivths fncggeffyc nstqlfnstw fnstwstegs nnategsdtt

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421 lpcrikqfin mwqevgkamy appisggirc ssnitgl11t rdggnnnngs eifrpqggdm
481 rdnwrselyk ykvvkieplg vaptkakrrv vqrekraevi galflgflga agstmgarsm
541 tlrvqarql1 sgivqqqnnl lraieaqqhl lqltvwgikq lqarilaver ylkdqql1gi
601 wgcsgklict tavpwnasws nksleqiwnn mtwmewdrei nnytslihs1 ieessqnqcek
661 negelleldk waslwnwfni tnwlwyikif imivgg1vg1 rivfavlsiv nrvrqgyspl
721 sfqth1ptpr gpdrpegeee eggerdrdrs irlvnngsl1 iwddllrs1cl fsyhr1rd11
781 livtrivell grrgweakly wwnllqywsq elknsvs11 nataiavaeg tdrvievvvqg
841 acrairhipr rirqgleril 1

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1: AAB59873. envelope polyprot...[gi:328559]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAB59873 856 aa linear VRL 01-OCT-1999
DEFINITION envelope polyprotein [Human immunodeficiency virus type 1].
ACCESSION AAB59873
VERSION AAB59873.1 GI:328559
DBSOURCE locus HIVPV22 accession K02083.1
KEYWORDS.
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.
REFERENCE 1 (residues 1 to 856)
AUTHORS Muesing,M.A., Smith,D.H., Cabradilla,C.D., Benton,C.V., Lasky,L.A. and Capon,D.J.
TITLE Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus
JOURNAL Nature 313 (6002), 450-458 (1985)
MEDLINE 85111157
PUBMED 2982104
REFERENCE 2 (sites)
AUTHORS van Beveren,C.P., Coffin,J. and Hughes,S.
TITLE Appendix B: HTLV-3/LAV genome
JOURNAL (in) Weiss,R.L., Teich,N., Varmus,H. and Coffin,J. (Eds.); RNA TUMOR VIRUSES, MOLECULAR BIOLOGY OF TUMOR VIRUSES, SECOND EDITION, 2: Supplements and Appendixes: 1106-1123; Cold Spring Harbor Laboratory, CSH, NY (1985)
COMMENT [1] revised sequence, personal communication.
[(in) Weiss,R., Teich,N., Varmus,H. and Coffin,J. (Eds.);RNA Tumor Viruses,Molecu] review; bases 1 to 9769.
[3] revises [1],[(in) Weiss,R., Teich,N., Varmus,H. and Coffin,J. (Eds.);RNA Tumor Viruses,Molecu].
This sequence for a H9/HTLV-III virus was determined from one complete proviral clone [1]. Additionally, several cDNA clones of the viral RNA were sequenced for comparison with the entire proviral sequence. The differences between cDNA and proviral DNA are extensive and are listed in the Sites Table as variations. The authors believe that the variations may be due in part to different strains in the H9/HTLV-III cell line, because it was established by infection with material from several AIDS patients. With the addition of g at 2111, gag cds and pol cds are very close to those of HXB2, BRU, and related HIV viruses.
For details and other references pertaining to Sites and Features, see the HIV reference entry.
Method: conceptual translation.
FEATURES
source Location/Qualifiers
1..856
/organism="Human immunodeficiency virus 1"
/proviral
/db_xref="taxon:11676"
Protein
1..856
/name="envelope polyprotein"
1..856
/coded_by="K02083.1:6267..8837"
CDS

ORIGIN

1 mrvkekyqhl wrwgwrwgtn llgmlmicsa teklwvtvyy gvpvwkeatt tlfcasdaka
61 ydtevhnvwa thacvptdpn pgevvlnvt enfnmwkndm veqmhedis lwdqslkpcv
121 kltplcvslk ctdlkndtnt nsssgrmyme kgeikncsfn istsirgkvq keyaffykld
181 iipidndtts ytltscntsv itqacpkvsf epipihycap agfailkcnn ktfngtgpc
241 nvstvqcthg irpvvstqll lngslaeee virsanftdn aktiivqlnq sveinctrpn
301 nntrksiriq rgpgrafvti gkignmrqah cnisrakwnn tlkqidsklr eqfgnnktii
361 fkqssggdpe ivthsfnccg effycnstql fnstwfinstw stegsnnteg sdtitlpc
421 kfqfinmwqev gkamyappis ggircssnit gllltrdggn nnnesEIFRP gggdmrdnwr
481 selykykvvk ieplgvaptk akrrrvvqrek ravgigalfl gflgaagstm gaasmrltvq
541 arqlsgivq qqnnllraie aqghllqltv wgikqlqari laverylkdq qllgiwgcs
601 klicttavpw naswsnksle qiwnnmwtwme wdreinnyts lihslieesq nqqekneqel
661 leldkwlanlw nwlnitnwlv yiklfimivg glvglrivfa vlsivnrvrq gysplsfqth
721 lptprgpdrp egieeedger drdrsirlvn gslaliwddl rslclfsyhr lrdlllivtr
781 ivellgrrgw ealkywwnll qywsqelkns avsllnatai avaegtdrvi evvqgayrai
841 rhiprrirqg lerill

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